



OIPE

RAW SEQUENCE LISTING

1 <110> APPLICANT: Kao, Hung-Teh

PATENT APPLICATION: US/09/929,313

DATE: 01/29/2002 TIME: 10:34:57

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         Hartig, Paul R.
         Branchek, Theresa
   <120> TITLE OF INVENTION: DNA Encoding A Human Serotonin (5-HT2) Receptor and
         Uses Thereof
 6 <130> FILE REFERENCE: 35997a3zy/JPW
 8 <140> CURRENT APPLICATION NUMBER: 09/929,313
 9 <141> CURRENT FILING DATE: 2001-08-14
11 <150> PRIOR APPLICATION NUMBER: US/09/145,864
12 <151> PRIOR FILING DATE: 1998-09-02
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         Ser Leu Met Gln Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn Asp Phe
30
                      20
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31
         aac too qqa qaa got aac act tot gat goa ttt aac tgg aca gto gac
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         Ser Glu Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys Leu Ser Pro Ser
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         Cys Leu Ser Leu Leu His Leu Gln Glu Lys Asn Trp Ser Ala Leu Leu
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         atg qca gtg tcc cta gag aaa aag ctg cag aat gcc acc aac tat ttc
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See See Lys Leu Cys Ala Val Trp Tle Tyr Leu Asp Val Leu Ple Ser Thr See Leu Leu		Pro		Ser	Met	Leu	Thr		Leu	Tyr	Gly	Tyr	-	Trp	Pro	Leu	Pro	
Ser Lys Leu Cys Ala Val Trp Ile Tyr Leu Asp Val Leu Phe Ser Thr				•														
145																		480
Sec tec atc atg cac ctc tgc gec atc teg ctg ctg	53	Ser	Lys	Leu	Cys	Ala		\mathtt{Trp}	Ile	Tyr	Leu	_	Val	Leu	Phe	Ser		
56 Ala Ser Ile Met His Leu Cys Ala Ile Ser Leu Asp Arg Tyr Val Ala 576 58 atc cag aac cac cac cac cgc ttc aac taag act aag cac aag cac cac aac tac tag gcc daa act atg gcc daa cac atg del fly leu																		
165	55				_				_		_	_	-	-			-	528
See	56	Ala	Ser	Ile	Met	His	Leu	Cys	Ala	Ile	Ser	Leu	Asp	Arg	Tyr	Val	Ala	
Tile Gin Asn Pro Tile His His Ser Arg Phe Asn Ser Arg Thr Lys Ala 180 180 185 180 180 185 190 180 185 190 180	57					165					170					175		
60																		576
61 ttt ctg aaa atc att gct gtt tgg acc ata tca gta ggt ata tcc atg 624 62 Phe Leu Lys Ile Ile Ala Val Trp Thr Ile Ser Val Gly Ile Ser Met 205 64 cca ata cca gtc ttt ggg cta cag gac gat tcg aag gtc ttt aag gag 672 65 Pro Ile Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu 210 66 210 225 67 ggg agt tgc tta ctt gcc gat gat aac ttt gtc ctg atc ggc tct ttt 720 68 Gly Ser Cys Leu Leu Ala Asp Asp Asp Phe Val Leu Ile Gly Ser Phe 225 69 225 230 70 gtg tca ttt ttc att ccc tta acc atc atg gtg atc acc tac ttt cta 768 71 Val Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu 225 73 act atc aag tca ctc cag aaa gaa gct act ttg tgt gta agt gat ctt 816 74 Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu 270 75 260 265 270 76 ggc aca cgg gcc aaa tta gct tct ttc agc ttc ctc cct cag agt tct 864 77 Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser 285 79 ttg ttc tc tca gaa agg ag cta tc tc cag cag tc	5.9	Ile	Gln	Asn	Pro	Ile	His	His	Ser	Arg	Phe	Asn	Ser	Arg	Thr	Lys	Ala	
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Cca ata cca gtc ttt ggg cta cag gac gat tcg aag gtc ttt aag gag G72	62	Phe	Leu	Lys	Ile	Ile	Ala	Val	${\tt Trp}$	Thr	Ile	Ser	Val	Gly	Ile	Ser	Met	
Pro Tie Pro Val Phe Gly Leu Gln Asp Asp Ser Lys Val Phe Lys Glu 210 2215 220 220 220 220 220 220 220 220 220 220 220 220 220 220 235 240	63			195					200					205				
66	64	cca	ata	cca	gtc	ttt	ggg	cta	cag	gac	gat	tcg	aag	gtc	ttt	aag	gag	672
67 ggg agt tgc tta ctt gcc gat gat aac ttt gtc ctg atc ggc tct ttt 720 68	6.5	Pro	Ile	${\tt Pro}$	Val	Phe	Gly	Leu	Gln	Asp	Asp	Ser	Ŀys	Val	Phe	Lys	Glu	
68	66		210					215					220					
69	67	ggg	agt	tgc	tta	ctt	gcc	gat	gat	aac	ttt	gtc	ctg	atc	ggc	tct	ttt	720
70	68	Gly	Ser	Cys	Leu	Leu	Ala	Asp	Asp	Asn	Phe	Val	Leu	Ile	Gly	Ser	Phe	
Yal Ser Phe Phe Ile Pro Leu Thr Ile Met Val Ile Thr Tyr Phe Leu	69	225					230					235					240	
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73 act atc aag tca ag tca cag aaa gaa gaa gaa gaa gaa gaa gaa g	71	Val	Ser	Phe	Phe	Ile	Pro	Leu	Thr	Ile	Met	Val	Ile	Thr	Tyr	Phe	Leu	
Thr Ile Lys Ser Leu Gln Lys Glu Ala Thr Leu Cys Val Ser Asp Leu 260	72					245					250					255		
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76 ggc aca cgg gcc aca tgg gcc aca tta gct tct ttc agc ttc ctc cct ccag agt tct 864 77 Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser 285 78 275 280 285 285 79 ttg tct tca gaa aag ctc ttc cag cgg tcg atc cat agg gag cca ggg 280 285 912 80 Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 295 300 912 81 290 295 300 300 960 82 tcc tac aca gg agg agg act atg ccg atg agg act atg ccg atg agg act agg act agg act agg agg act agg act agg agg act agg agg act agg agg act agg act agg act agg act agg act agg agg act a	74	Thr	Ile	Lys	Ser	Leu	Gln	Lys	Glu	Ala	Thr	Leu	Cys	Val	Ser	Asp	Leu	
77 Gly Thr Arg Ala Lys Leu Ala Ser Phe Ser Phe Leu Pro Gln Ser Ser 275	75				260					265					270			
78 ttg tct tca gaa aag ctc ttc cag cgg tcg atc cat agg gag cca ggg 912 80 Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 295 81 290 10	76	ggc	aca	cgg	gcc	aaa	tta	gct	tct	ttc	agc	ttc	ctc	cct	cag	agt	tct	864
79 ttg tct tca gaa aag ctc ttc cag cgg tcg atc cat agg gag cca ggg 912 80 Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 81 290 295 300 82 tcc tac aca ggc agg agg act atg cag tcc atc agc aat gag caa aag 960 83 Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys 84 305 310 315 320 85 gca tgc aag gtg ctg ggc atc gtc ttc ttc ttc ctg ttt gtg gtg atg tgg 1008 86 Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp 330 335 88 tgc cct ttc ttc atc aca aac acc acc acc ac	77	Gly	Thr	Arg	Ala	Lys	Leu	Ala	Ser	Phe	Ser	Phe	Leu	Pro	Gln	Ser	Ser	
Leu Ser Ser Glu Lys Leu Phe Gln Arg Ser Ile His Arg Glu Pro Gly 290 295 300 300 82 100 1	78			275					280					285				
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Ser Tyr Thr Gly Arg Arg Thr Met Gln Ser Ile Ser Asn Glu Gln Lys 305 310 310 315 320 85 gca tgc aag gtg ctg ggc atc gtc ttc ttc ctg ttt gtg gtg atg tgg 1008 86 Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp 87 325 330 335 88 tgc cct ttc ttc atc aca aac atc atg gcc gtc atc tgc aaa gag tcc 1056 89 Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser 90 340 345 350 91 tgc aat gag gat gtc att ggg gcc ctg ctc aat gtg ttt gtt tgg atc 1104 92 Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile 93 355 360 365 94 ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac 1152 95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	81		290					295					300					
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86 Ala Cys Lys Val Leu Gly Ile Val Phe Phe Leu Phe Val Val Met Trp 87 325 330 335 88 tgc cct ttc ttc atc aca aac atc atg gcc gtc atc tgc aaa gag tcc 1056 89 Cys Pro Phe Phe Ile Thr Asn Ile Met Ala Val Ile Cys Lys Glu Ser 90 340 345 350 91 tgc aat gag gat gtc att ggg gcc ctg ctc aat gtg ttt gtt tgg atc 1104 92 Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile 93 355 360 365 94 ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac 1152 95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	84	305					310					315					320	
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Cys Asn Glu Asp Val Ile Gly Ala Leu Leu Asn Val Phe Val Trp Ile 355 360 365 94 ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac 95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	90				340					345					350			
93 355 360 365 94 ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac 1152 95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	91	tgc	aat	gag	gat	gtc	att	ggg	gcc	ctg	ctc	aat	gtg	ttt	gtt	tgg	atc	1104
93 355 360 365 94 ggt tat ctc tct tca gca gtc aac cca cta gtc tac aca ctg ttc aac 1152 95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	92																	
95 Gly Tyr Leu Ser Ser Ala Val Asn Pro Leu Val Tyr Thr Leu Phe Asn	93	_			_			_										
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	106 107 108		_		-	gcc Ala	aag	aca		_	aat	gac Asp	_		atg	gtt	_		1344
	109 110 111			_	cag Gln	cat		-		gct Ala		aaa Lys	-		āgc	-			1392
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	137 138				115					120		Gly		_	125				
	139 140			130					135			Leu		140					
	141		145		L Cu	0,0		150		110	-1-	Leu	155	, u i	ЦСи	1 110	001	160	
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207					85					90					95	
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219	110	01		180	110		*****	001	185	1 110			9	190	-10	
220	Dhe	T.e.11	T.vc		Tle	Δla	Val	Trn		Tle	Ser	Va1	Glv		Ser	Met
221	1110	пси	195	110	110	211u	val	200	1111	110	UCI	Val	205	110	DCI	1100
222	Dro	Tlo		17a l	Dho	C117	Leu		λen	Nen	Sar	Laze		Dha	Lve	Glu
223	PIO	210	PIO	Val	PHE	GIY	215	GIII	АЗР	ASP	261	220	Val	rne	цуз	GIU
	C1**		C	T 011	Ton	λla		λαν	λan	Dho	17 a 1		т1.	C1**	cor	Dho
224	_	261	Cys	ьеи	ьeu		Asp	ASP	ASII	Pile		ьeu	116	СТУ	ser	240
225	225	21-	Dho	Dho	т1.	230	T 011	mb∽	т1.	Wot	235	т1.	mh ~	m	Dho	
226	val	Ата	Pne	Pne		Pro	Leu	THE	тте		val	тте	THE	TAL		Leu
227	m1	~1 -	•	a	245	a1	.	01	. 1 -	250	T	a	17- 1	a	255	T
228	Thr	тте	ràs		ьeu	GIN	Lys	GIU		Tnr	Leu	Cys	vaı		Asp	Leu
229	_	1		260	_	_		_	265	_	-1	_	_	270	_	_
230	ser	Thr	_	Ala	гàг	Leu	Ala		Pne	ser	Pne	Leu		GIn	ser	Ser
231			275	_				280		_	_		285		_	
232	Leu		Ser	Glu	Lys	Leu	Phe	Gln	Arg	Ser	Ile		Arg	Glu	Pro	GTA
233		290					295		_			300			_	
234		Tyr	Ala	Gly	Arg	_	Thr	Met	Gln	Ser		Ser	Asn	Glu	Gln	
235	305					310					315					320
236	Ala	Cys	Lys	Val		Gly	Ile	Val	Phe		Leu	Phe	Val	Val		\mathtt{Trp}
237					325					330					335	
238	Cys	Pro	Phe	Phe	Ile	Thr	Asn	Ile	Met	Ala	Val	Ile	Cys	Lys	Glu	Ser
239				340					345					350		
240	Cys	Asn	Glu	Asn	Val	Ile	Gly	Ala	Leu	Leu	Asn	Val	Phe	Val	Trp	Ile
241			355					360					365			
242	Gly	Tyr	Leu	Ser	Ser	Ala	Val	Asn	${\tt Pro}$	Leu	Val	Tyr	Thr	Leu	Phe	Asn
243		370					375					380				
244	Lys	Thr	Tyr	Arg	Ser	Ala	Phe	Ser	Arg	Tyr	Ile	Gln	Cys	Gln	Tyr	Lys
245	385					390		٠, .			395					400
246	Glu	Asn	Arg	Lys	Pro	Leu	Gln	Leu	Ile	Leu	Val	Asn	Thr	Ile	Pro	Ala

VERIFICATION SUMMARY

DATE: 01/29/2002

PATENT APPLICATION: US/09/929,313

TIME: 10:34:58

Input Set : N:\Crf3\RULE60\09929313.raw
Output Set: N:\CRF3\01292002\I929313.raw

L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1